

Figure 1. Nucleotide and amino acid sequence of Mgp002 from *Chlamydia muridium*.

atg gga tta tct cgc cta att tta ttt ggc tta ctt tct tta ccg ctc	48
Met Gly Leu Ser Arg Leu Ile Leu Phe Gly Leu Leu Ser Leu Pro Leu	
1 5 10 15	
↓	
tca gca agc tgc gac ttc ccc ccc agt gtt tcc cag aag ata tta ttc	96
Ser Ala Ser Cys Asp Phe Pro Pro Ser Val Ser Gln Lys Ile Leu Phe	
20 25 30	
ttg tgt caa aaa tct att cct caa gct ctg gag tcc tat ctt gag gca	144
Leu Cys Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala	
35 40 45	
tct aca acc tat caa caa cat aac ttt tct ata ttg cgc tta ata gct	192
Ser Thr Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala	
50 55 60	
aag tca tac tta caa caa agt ctc ttt tct gaa gat gct tac gta cgc	240
Lys Ser Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg	
65 70 75 80	
aaa agc gca att att gga gcg ggg ctt tct ggc tca tct gag act cta	288
Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu	
85 90 95	
gat cta ctg tct gaa tcc ata gaa aca cag gat ctt tat gag cag cta	336
Asp Leu Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu	
100 105 110	
ctt att tta aat gct gca ggc aat caa tta ggc aaa act tcc gat cgt	384
Leu Ile Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg	
115 120 125	
ctt tta ttc aaa gga tta aca gca cct cat cct att att cgc ttg gaa	432
Leu Leu Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu	
130 135 140	
gct gct tac cgt ctg gcc tgt atg aaa aac agt aaa gta agt gac tac	480
Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr	
145 150 155 160	
ctc tat tct ttt atc cac cag ctt cca gaa gaa atc caa aac tta gca	528
Leu Tyr Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala	
165 170 175	
gca acg att ttt ttg cag ctc gaa acg gaa gaa gca gat gct tat gtt	576
Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val	
180 185 190	
cat aga ctc ctg tct tct cct aat agt cta aca aga aac tat atg gct	624
His Arg Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala	
195 200 205	
tat cta att gga gaa tat caa cag agg aga ttt ctt cca acg ctc cgc	672
Tyr Leu Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg	
210 215 220	
tcg ttg ctt acc agc gca gct cct tta gac caa gaa gga tct ttg tat	720
Ser Leu Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr	
225 230 235 240	

gct ata gga aaa tta gaa gat gcc agc agc tat cct aaa atc aaa gca Ala Ile Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala 245 250 255	768
tta agc tcc aaa tct aac cct gaa gtg gct ctt gct gct gct cag aca Leu Ser Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Gln Thr 260 265 270	816
tta tta ttc ttg ggt aaa gaa gat gag gct ctt cct atc cta act act Leu Leu Phe Leu Gly Lys Glu Asp Glu Ala Leu Pro Ile Leu Thr Thr 275 280 285	864
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att aaa gaa gaa att aaa ctg aat gct gct ttg gct ctt gtc cac ttg Ile Lys Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu 325 330 335	1008
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aat aaa att ctc cac cgc ata ttt tta ccc acc cat tcg ata gga aaa Asn Lys Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys 355 360 365	1104
gcc acg cag ttt tgg aaa gag tgt acg gca ctc cct ctt cta agc cca Ala Thr Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro 370 375 380	1152
gaa gaa aaa gca aga gct ttg gca atg tat cgc gca gca gaa gat acg Glu Glu Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr 385 390 395 400	1200
atc ctc tct agt tta tta aaa tta cct aac aat gcc tat ctg cct tat Ile Leu Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr 405 410 415	1248
ttg gaa cgt att cta act tca caa aaa acc cct cta gca gct aaa gct Leu Glu Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala 420 425 430	1296
att gct ttt tta tca gta aca gct cat cct cag gca ctt tct tta gtc Ile Ala Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val 435 440 445	1344
tcg aaa gca gca cta act cca gga gac cct atc att cgc gct tat gcg Ser Lys Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala 450 455 460	1392
aat tta gct tta tat aca atg acg caa gat cct gaa aag aaa gcc tta Asn Leu Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu 465 470 475 480	1440
tta tat caa tat gcc gaa cag tta ata gga gac acg att ttg ttt aca Leu Tyr Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr	1488

485										490					495					
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Asp	Glu	Glu	Asn	Pro	Leu	Pro	Ser	Pro	His	Ser	Ser	Tyr	Leu	Arg	Tyr					
			500					505					510							
caa	gtg	tcc	cca	gaa	act	cgt	tct	caa	ctc	atg	cta	act	att	tta	gaa	1584				
Gln	Val	Ser	Pro	Glu	Thr	Arg	Ser	Gln	Leu	Met	Leu	Thr	Ile	Leu	Glu					
		515					520					525								
acc	cta	gtt	tct	tct	aaa	act	gat	gaa	gac	atc	cga	gtt	ttt	ott	tcg	1632				
Thr	Leu	Val	Ser	Ser	Lys	Thr	Asp	Glu	Asp	Ile	Arg	Val	Phe	Leu	Ser					
		530				535					540									
cta	atg	aaa	aaa	acc	cat	tac	aaa	aat	atc	ccc	atc	tta	tct	gga	tta	1680				
Leu	Met	Lys	Lys	Thr	His	Tyr	Lys	Asn	Ile	Pro	Ile	Leu	Ser	Gly	Leu					
545					550				555					560						
tta	atg	aga	ata	gtg	gag											1698				
Leu	Met	Arg	Ile	Val	Glu															
				565																

Figure 2. *C. trachomatis* equivalent Mgp002 nucleic acid and amino acid sequence.

atg gga cta tct cgt cta gcc ttc att agt ttc ctc tct ttt aca ctc	48
Met Gly Leu Ser Arg Leu Ala Phe Ile Ser Phe Leu Ser Phe Thr Leu	
1 5 10 15	
↓	
tca gcc agc tgt gat ttt cct tcc tca gtt tct cag aga atc ttg ttt	96
Ser Ala Ser Cys Asp Phe Pro Ser Ser Val Ser Gln Arg Ile Leu Phe	
20 25 30	
tct tgc cga aaa tca gtc cct caa gct cta gaa gcc tat ctc gaa gct	144
Ser Cys Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala	
35 40 45	
tca gca act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca	192
Ser Ala Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala	
50 55 60	
gaa tcg tat tta caa caa agc ttt ctc tct gag gac acc tac ata cgt	240
Glu Ser Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg	
65 70 75 80	
aaa agt gca att att gga gca ggg cta tct ggt tca tca gaa gct tta	288
Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu	
85 90 95	
gag tta ctg tct gag gct ata gaa acg caa gat ctc tat gag caa cta	336
Glu Leu Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu	
100 105 110	
ctc att tta aat gct gca acc agc caa tta agc aaa act tct gac aaa	384
Leu Ile Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys	
115 120 125	
ctt tta ttc aag gga tta aca gct tct cat cct gtc atc cgc tta gaa	432
Leu Leu Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu	
130 135 140	
gct gct tat cgt ctt gcc tgt atg aaa aat agc aag gta agt gat tac	480
Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr	
145 150 155 160	
ctt tat tct ttt atc tac aag tta cca gaa gaa att caa aac cta gcg	528
Leu Tyr Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala	
165 170 175	
gca act att ttc tta caa ctc gaa aca gaa gaa gct gat gct tat att	576
Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile	
180 185 190	
cat cat ttg ctc tct tct ccc aat aac ctg aca aga aac tat gtt gcc	624
His His Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala	
195 200 205	
tat tta att gga gag tac aaa caa aaa aga ttt ctt cca aca cta cgc	672
Tyr Leu Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg	
210 215 220	
tct tta ctt aca agt gcc tct cct tta gat caa gaa ggc gct ttg tat	720
Ser Leu Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr	
225 230 235 240	

gcg tta ggc aaa ctg gaa gac tct ggt agc tat cct aga att aaa gct Ala Leu Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala 245 250 255	768
cta agc tct aga tcc aat cct gaa gta gta ctc gct gca gct cag aca Leu Ser Ser Arg Ser Asn Pro Glu Val Leu Ala Ala Gln Thr 260 265 270	816
tta tta ttc tta gag aaa gaa gaa gaa gct cta ccg atc cta acc aac Leu Leu Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn 275 280 285	864
ctt tgc caa caa aaa ctt ctt cga gcc ctg tat acc gca cgt ttc ctc Leu Cys Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu 290 295 300	912
tcg caa gag aag ggt gaa gag ctt ctt ctt cca atc ttt tat aac gca Ser Gln Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala 305 310 315 320	960
aca caa gaa gaa att aga ctg aat act gct tta gca ctt gtt cat caa Thr Gln Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln 325 330 335	1008
ggg tgt aca gat cct caa gtc ctc cac tat cta aca gaa atc tta gaa Gly Cys Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu 340 345 350	1056
agt aaa gtt ctc cat cgc ata ttt tta cct act cac tcg aca gga aaa Ser Lys Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys 355 360 365	1104
gct ata cag ttc tgg aaa gaa tgc acc act ttt cct ctc atg agc caa Ala Ile Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln 370 375 380	1152
gaa gac aaa atg aga acg ttg gct atg tat cgg gta gcg gaa gat acc Glu Asp Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr 385 390 395 400	1200
atc ctc tca gcg tta cta aaa tta ccc aat gac gcc tat ctt cct tac Ile Leu Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr 405 410 415	1248
cta gag cgc atc ctc gcc tca caa aaa act ata cta gca gct aaa gct Leu Glu Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala 420 425 430	1296
att gct ttt tta tcg gta aca gct cat cct cag gca ctt tct tta gtc Ile Ala Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val 435 440 445	1344
tcg aaa gct gca tta act cct gga gac cct atc att cgc gct tac gct Ser Lys Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala 450 455 460	1392
aat cta gct tta tat aca atg acc aaa gat cct gag aaa aaa gct gtg Asn Leu Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val 465 470 475 480	1440
cta tac cga tat gct gaa caa tta ata gag gat acc att tta ttc aca Leu Tyr Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr	1488

485										490										495										
gat	gct	gaa	aat	ccg	ctt	ccc	tct	cca	agc	tct	tct	tat	tta	cgc	tac	1536														
Asp	Ala	Glu	Asn	Pro	Leu	Pro	Ser	Pro	Ser	Ser	Ser	Tyr	Leu	Arg	Tyr															
500					505					510																				
caa	gta	tcc	cct	gag	acc	cgc	aca	caa	ctt	atg	cta	gct	att	ttg	gaa	1584														
Gln	Val	Ser	Pro	Glu	Thr	Arg	Thr	Gln	Leu	Met	Leu	Ala	Ile	Leu	Glu															
515					520					525																				
acc	tta	ggt	tct	tcc	aaa	acg	gat	gaa	gat	atc	cgc	ggt	ttt	ctt	tcc	1632														
Thr	Leu	Val	Ser	Ser	Lys	Thr	Asp	Glu	Asp	Ile	Arg	Val	Phe	Leu	Ser															
530					535					540																				
cta	atg	aaa	aaa	acc	cat	tac	aaa	aat	atc	ccg	atc	tta	tca	gga	ttg	1680														
Leu	Met	Lys	Lys	Thr	His	Tyr	Lys	Asn	Ile	Pro	Ile	Leu	Ser	Gly	Leu															
545					550					555					560															
tta	atg	aga	ata	gtg	gag											1698														
Leu	Met	Arg	Ile	Val	Glu																									
565																														

Figure 3. Immunization protocol.

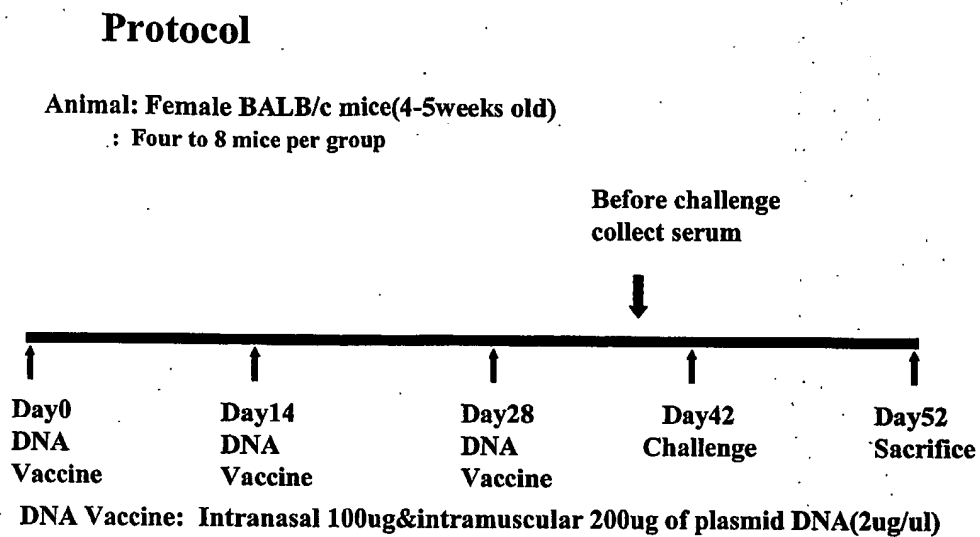
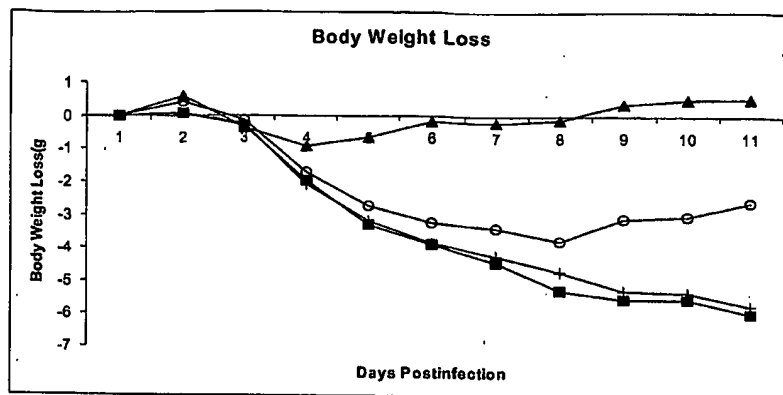
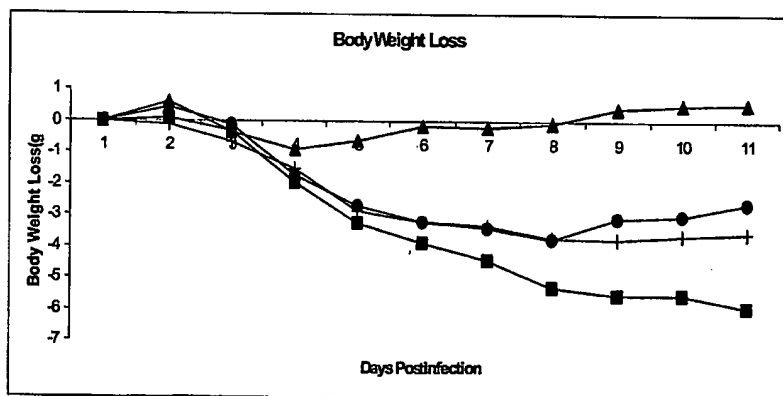


Figure 4. Body Weight loss after immunization.

Panel A Mgp002 full-length



Panel B Mgp002 signal sequence deleted



▲ - EB

○ - pCACT Mgp002

● - pCACT Mgp002delta

+ - pCAMycHis

■ - Naive

Figure 6. Recombinant Protein Expression of Mgp002.

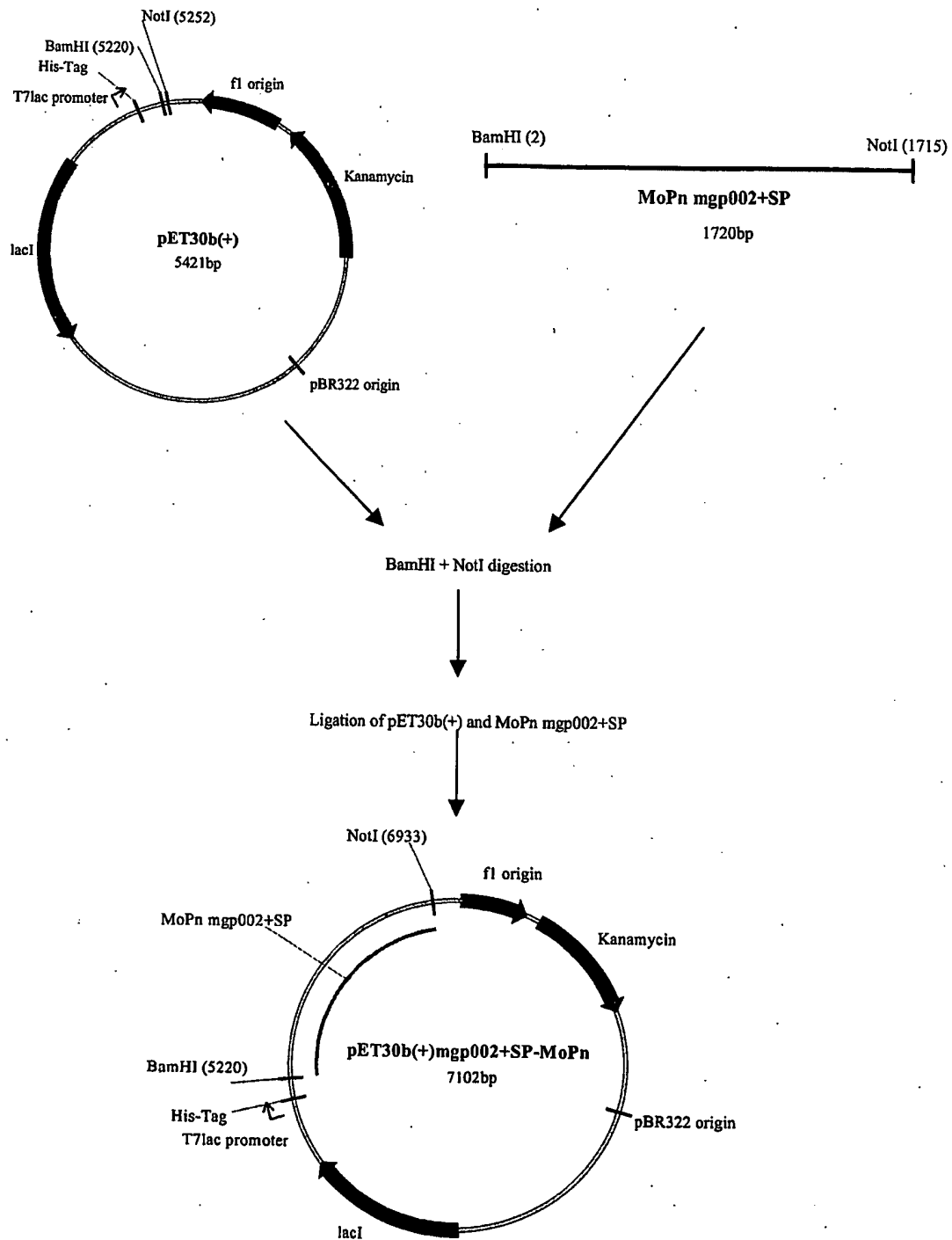
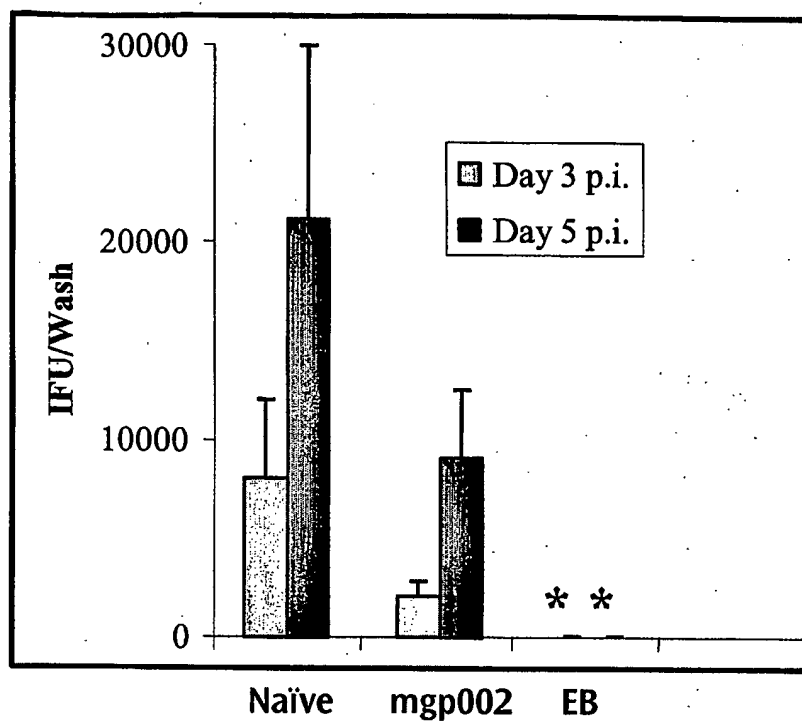
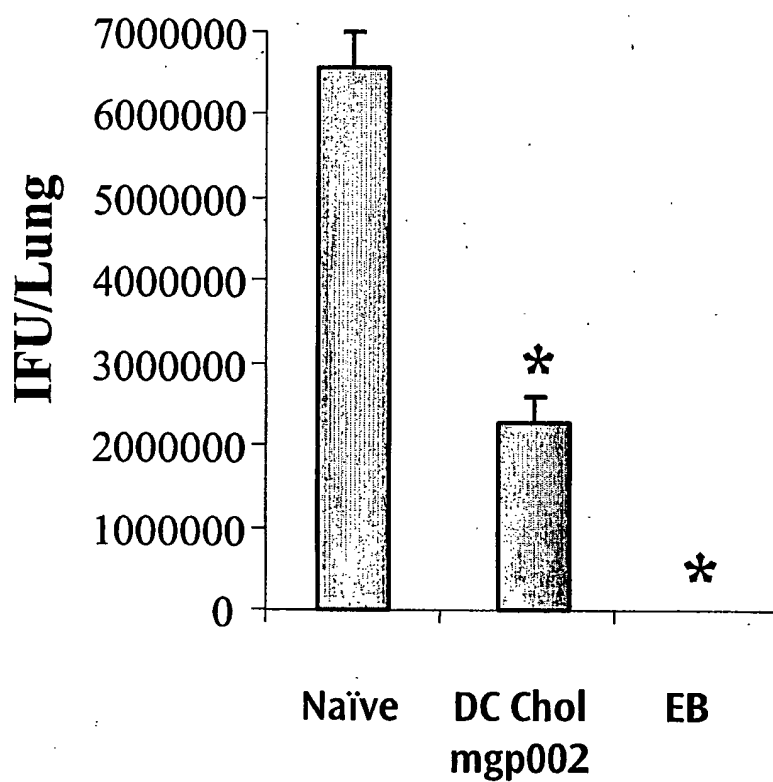


Figure 7. Protection from *C. trachomatis* Serovar D Challenge.

* Wilcoxon $p < .05$

Figure 8. Chlamydial Lung Burden Following MoPn Intranasal Challenge in Mpg002 immunized mice.



•Wilcoxon $p < .05$